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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/017,372C

DATE: 06/28/2002

TIME: 14:12:02

Input Set : A:\61302updated.ST25.txt

Output Set: N:\CRF3\06282002\J017372C.raw

3 <110> APPLICANT: Wolfrain, Lawrence A
4 Letterio, John J
6 <120> TITLE OF INVENTION: FUNCTIONALIZED TGF-BETA FUSION PROTEINS
8 <130> FILE REFERENCE: 4239-61302
10 <140> CURRENT APPLICATION NUMBER: US 10/017,372C
11 <141> CURRENT FILING DATE: 2001-10-19
13 <150> PRIOR APPLICATION NUMBER: US 60/242,292
14 <151> PRIOR FILING DATE: 2000-10-20
16 <160> NUMBER OF SEQ ID NOS: 39
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 28
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Primer
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33 <211> LENGTH: 42
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35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
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47 <213> ORGANISM: Artificial Sequence
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57 <211> LENGTH: 45
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59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Primer
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65 cttgtcgtcg tcatccttgt agtctcggcg gtgccgggag ctgtg 45
68 <210> SEQ ID NO: 5

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73 <220> FEATURE:
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83 <213> ORGANISM: Artificial Sequence
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86 <223> OTHER INFORMATION: Primer
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94 <212> TYPE: PRT
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Synthetic oligopeptide
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108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
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114 <220> FEATURE:
115 <221> NAME/KEY: CDS
116 <222> LOCATION: (1)..(1197)
117 <223> OTHER INFORMATION:
120 <220> FEATURE:
121 <221> NAME/KEY: misc_feature
122 <222> LOCATION: (278)..(279)
123 <223> OTHER INFORMATION: Maturation cleavage site
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127 atg gcg cct tcg ggg ctg cgg ctc ttg ccg ctg ctg ctg ccg ctg ctg 48
128 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
129 1 5 10 15
131 tgg ctg cta gtg ctg acg cct ggc cgg ccg gcc gcc gga ctg tcc acc 96
132 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
133 20 25 30
135 tgc aag acc atc gac atg gag ctg gtg aag cgg aag cgc atc gag gcc 144
136 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
137 35 40 45
139 att cgc ggc cag att ctg tcc aag ctt cgg ctt gcc agc ccc ccg agc 192

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140 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
141      50                      55                      60
143 cag ggg gac gtg ccg ccc ggc ccg ctg cct gag gca gta ctg gct ctt      240
144 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
145 65                      70                      75                      80
147 tac aac agt acc cgc gac cgg gta gcc ggg gaa agt gtc gaa ccg gag      288
148 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
149                      85                      90                      95
151 ccc gag cca gag gcg gac tac tac gcc aag gag gtc acc cgc gtg cta      336
152 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
153      100                      105                      110
155 atg gtg gaa agc ggc aac caa atc tat gat aaa ttc aag ggc acc ccc      384
156 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
157      115                      120                      125
159 cac agc tta tat atg ctg ttc aac acg tcg gag ctc cgg gaa gcg gtg      432
160 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
161      130                      135                      140
163 ccg gaa cct gta ttg ctc tct cgg gca gag ctg cgc ctg ctg agg ctc      480
164 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
165 145                      150                      155                      160
167 aag tta aaa gtg gag cag cac gtg gag cta tac cag aaa tac agc aat      528
168 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
169      165                      170                      175
171 gat tcc tgg cgc tac ctc agc aac cgg ctg ctg gcc ccc agt gac tca      576
172 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
173      180                      185                      190
175 ccg gag tgg ctg tcc ttt gat gtc acc gga gtt gtg cgg cag tgg ctg      624
176 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
177      195                      200                      205
179 acc cgc aga gag gct ata gag ggt ttt cgc ctc agt gcc cac tct tcc      672
180 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
181      210                      215                      220
183 tct gac agc aaa gat aac aca ctc cac gtg gaa att aac ggg ttc aat      720
184 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
185 225                      230                      235                      240
187 tct ggc cgc cgg ggt gac ctg gcc acc att cac ggc atg aac cgg ccc      768
188 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
189      245                      250                      255
191 ttc ctg ctc ctc atg gcc acc ccg ctg gag agg gcc cag cac ctg cac      816
192 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
193      260                      265                      270
195 agc tcc cgg cac cgc cga gac tac aag gat gac gac gac aag gcc ctg      864
196 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
197      275                      280                      285
199 gat acc aac tac tgc ttc agc tcc acg gag aag aac tgc tgc gtg cgg      912
200 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
201      290                      295                      300
203 cag ctc tac att gac ttc cgg aag gac ctg ggc tgg aag tgg att cat      960
204 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His

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205 305          310          315          320
207 gaa ccc aag ggc tac cat gcc aat ttc tgc ctg ggg ccc tgt ccc tac      1008
208 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
209          325          330          335
211 atc tgg agc cta gac act cag tac agc aag gtc ctg gct ctg tac aac      1056
212 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
213          340          345          350
215 cag cac aac ccg ggc gcg tcg gcg gcg ccg tgc tgc gtg ccg cag gcg      1104
216 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
217          355          360          365
219 ctg gag cca ctg ccc atc gtg tac tac gtg ggc cgc aag ccc aag gtg      1152
220 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
221          370          375          380
223 gag cag ctg tcc aac atg atc gtg cgt tcc tgc aag tgc agc tga      1197
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225 385          390          395
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229 <211> LENGTH: 398
230 <212> TYPE: PRT
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Fusion oligonucleotide
236 <220> FEATURE:
237 <221> NAME/KEY: misc_feature
238 <222> LOCATION: (278)..(279)
239 <223> OTHER INFORMATION: Maturation cleavage site
241 <400> SEQUENCE: 9
243 Met Ala Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu
244 1          5          10          15
247 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr
248          20          25          30
251 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala
252          35          40          45
255 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser
256          50          55          60
259 Gln Gly Asp Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu
260 65          70          75          80
263 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Val Glu Pro Glu
264          85          90          95
267 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu
268          100          105          110
271 Met Val Glu Ser Gly Asn Gln Ile Tyr Asp Lys Phe Lys Gly Thr Pro
272          115          120          125
275 His Ser Leu Tyr Met Leu Phe Asn Thr Ser Glu Leu Arg Glu Ala Val
276          130          135          140
279 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu
280 145          150          155          160
283 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn
284          165          170          175

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287 Asp Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser
288          180          185          190
291 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu
292          195          200          205
295 Thr Arg Arg Glu Ala Ile Glu Gly Phe Arg Leu Ser Ala His Ser Ser
296          210          215          220
299 Ser Asp Ser Lys Asp Asn Thr Leu His Val Glu Ile Asn Gly Phe Asn
300 225          230          235          240
303 Ser Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro
304          245          250          255
307 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu His
308          260          265          270
311 Ser Ser Arg His Arg Arg Asp Tyr Lys Asp Asp Asp Asp Lys Ala Leu
312          275          280          285
315 Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys Val Arg
316          290          295          300
319 Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp Ile His
320 305          310          315          320
323 Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr
324          325          330          335
327 Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr Asn
328          340          345          350
331 Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro Gln Ala
332          355          360          365
335 Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro Lys Val
336          370          375          380
339 Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
340 385          390          395

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343 <210> SEQ ID NO: 10

344 <211> LENGTH: 362

345 <212> TYPE: DNA

346 <213> ORGANISM: Artificial Sequence

348 <220> FEATURE:

349 <223> OTHER INFORMATION: Fusion oligonucleotide

351 <400> SEQUENCE: 10

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356 attcatgaac ccaagggctc catgccatt tctgcctggg gccctgtccc tacatctgga      180
358 gcctagacac tcagtacagc aaggtcctgg ctctgtacaa ccagcacaac ccgggcgcgt      240
360 cggcggcgcc gtgctgcgtg ccgcaggcgc tggagccact gcccatcgtg tactacgtgg      300
362 gccgcaagcc caaggtggag cagctgtcca acatgatcgt gcgttctgc aagtgcagct      360
364 ga

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367 <210> SEQ ID NO: 11

368 <211> LENGTH: 120

369 <212> TYPE: PRT

370 <213> ORGANISM: Artificial Sequence

372 <220> FEATURE:

373 <223> OTHER INFORMATION: Fusion oligopeptide

375 <220> FEATURE:

VERIFICATION SUMMARY

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PATENT APPLICATION: US/10/017,372C

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